Compositional analysis of high throughput sequencing data

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Chapter 1

About this document

This document is an .Rmd document and can be found at:

github.com/ggloor/book

The generation of this document requires `R` and an installation of LaTeX to work properly. This document contains interspersed markdown and `R` code that may be compiled into a pdf document and supports the figures and assertions in the main article. `R` code is (almost always) exposed in the pdf document so that the interested reader can work through the example code themselves. Code that is not exposed is in the `chunk` directory.

Reproducing the analysis

From an R command prompt you can compile this document into PDF if you have LaTeX and pandoc installed:

`bookdown::render_book("index.Rmd")` or you can open the file in RStudio and compile in that environment.

R packages required

We will need the following R packages, several functions are defined in a dedicated functions section.

1. knitr (CRAN)
2. bookdown (CRAN)
3. vegan (CRAN)